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DISEASE NOTE

First report of grapevine virus E infecting grapevine in Argentina

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Grapevine is the most important fruit crop in Argentina in terms of cultivated area, as well as production volume. To date, only 11 viruses have been reported to infect vine in Argentina (Lanza Volpe et al. 2015).

Grapevine virus E (GVE) is a member of the genus *Vitivirus* in the family *Betaflexiviridae* (Alabi et al. 2013; Nakaune et al. 2008), which was tentatively linked with the rugose wood complex disease (Al Rwahnih et al. 2012). To investigate the occurrence of GVE in Argentina, a survey was conducted in grapevines from three regions (Mendoza's North Oasis, East Zone and Uco Valley) of Mendoza province, Argentina, during the 2017/2018 season. A total of 187 plants were screened, including *Vitis vinifera* Malbec, Cot, Cabernet franc, Cereza, Aspirant Bouchet, Chardonnay, Flame and Paulsen 1103 rootstock (*V. berlandieri* cv. Rességuier x *V. rupestris* cv. Lot). Total RNA from cambial scrapings of all samples were purified by Spectrum Plant Total RNA Kit (Sigma-Aldrich, USA), reverse transcribed using random primers (6-mers) and tested by RT-PCR using primers Fw:TCTTTCGAACYGAAGGTGCCA and Rv:GGGTCAATCAACCAACATGC, which were designed for the amplification of a 466 bp fragment of a conserved region spanning part of the coat protein and NAB proteins CDS of GVE or grapevine virus L (GVL) (Debat et al. 2018). Results showed that two of the tested samples (belonging to the Paulsen 1103 rootstock) tentatively presented GVE/GVL RNA. To confirm the identity of the RT-PCR positive samples, the products were cloned, bi-directionally Sanger sequenced and compared with GenBank available sequences. The partial nucleotide sequences sharing a 98.7% pairwise identity were deposited as (MH580899, P3-MZ) and (MH580900, P5-MZ), showing highest identities ranging from 98.3 to 98.7% with the GVE reference genome sequence isolated from *V. labruscana* cv. Aki Queen in Japan (TvAQ7, AB432910) and only 79.5% with GVL (isolate RI, MH248020). To further support our findings we tested the samples with additional primers Fw: GTTCAGAT GCCAAAGCTGGG and Rv: GGCCCAATTGATAG CGGAGA, which allowed the amplification, cloning and sequencing of a 435 nt fragment of the replicase encoding region of the virus. The resulting sequences shared a 99.2% pairwise identity and presented a 97% (MK561024, P5-MZ) and 97.7% (MK561025, P3-MZ) highest identity with GVE TvAQ7, confirming that the detected virus corresponded to GVE. The Argentinean isolates of GVE were found in plants not showing any obvious symptoms of viral diseases. To our knowledge, this is the first report of GVE in Argentinian grapevines, which motivates its inclusion among the viruses considered in the grapevine certification scheme of Argentina.

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